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TECH CENTER 1600/2900

<120> Novel Tumor-Associated Marker

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<170> PatentIn version 3.1

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<211> 912

<212> PRT

<213> Human

<400> 8

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Gln Glu Asp Asp Trp Asp Arg Asp Leu Leu Leu Asp Pro Ala Trp Glu
35 40 45

Lys Gln Gln Arg Lys Thr Phe Thr Ala Trp Ser Asn Ser His Leu Arg
50 55 60

Lys Ala Gly Thr Gln Ile Glu Asn Ile Asp Glu Asp Phe Arg Asp Gly
65 70 75 80

Leu Lys Leu Met Leu Leu Leu Glu Phe Ile Ser Gly Glu Arg Leu Pro
85 90 95

Lys Pro Glu Arg Gly Lys Met Arg Val His Lys Ile Asn Asn Val Asn
100 105 110

Lys Ala Leu Asp Phe Ile Ala Ser Lys Gly Ile Lys Leu Asp Phe His
115 120 125

Arg Ala Glu Glu Ile Val Asp Gly Asn Ala Lys Met Thr Leu Gly Met
130 135 140

Ile Trp Thr Ile Ile Leu Arg Phe Ala Ile Gln Asp Ile Ser Val Glu
145 150 155 160

Glu Thr Ser Ala Lys Glu Gly Leu Leu Leu Trp Cys Gln Arg Lys Thr
165 170 175

B1
Cont

Ala Pro Tyr Lys Asn Val Asn Val Gln Asn Phe His Ile Ser Trp Lys
180 185 190

Asp Gly Leu Ala Phe Asn Ala Leu Ile His Arg His Arg Pro Glu Leu
195 200 205

Ile Glu Tyr Asp Lys Leu Arg Lys Asp Asp Pro Val Thr Asn Leu Asn
210 215 220

Asn Ala Phe Glu Val Ala Glu Lys Tyr Leu Asp Ile Pro Lys Met Leu
225 230 235 240

Asp Ala Glu Asp Ile Val Asn Thr Ala Arg Pro Asp Glu Lys Ala Ile
245 250 255

Met Thr Tyr Val Ser Ser Phe Tyr His Ala Phe Ser Gly Ala Gln Lys
260 265 270

Ala Glu Thr Glu Thr Ala Ala Asn Arg Ile Cys Lys Val Leu Ala Val
275 280 285

Asn Gln Glu Asn Cys Ser Thr Ser Met Glu Asp Tyr Glu Lys Leu Ala
290 295 300

Ser Asp Leu Leu Glu Trp Ile Arg Arg Thr Ile Pro Trp Leu Glu Asp
305 310 315 320

Arg Val Pro Gln Lys Thr Ile Gln Glu Met Gln Gln Lys Leu Glu Asp
325 330 335

Phe Arg Asp Tyr Arg Arg Val His Lys Pro Pro Lys Val Gln Glu Lys
340 345 350

Cys Gln Leu Glu Ile Asn Phe Asn Ser Val Gln Thr Lys Leu Arg Leu
355 360 365

Ser Asn Arg Pro Ala Phe Met Pro Ser Glu Gly Lys Met Val Ser Asp
370 375 380

Ile Asn Asn Gly Trp Gln His Leu Glu Gln Ala Glu Lys Gly Tyr Glu
385 390 395 400

Glu Trp Leu Leu Asn Glu Ile Arg Arg Leu Glu Arg Leu Asp His Leu
405 410 415

Ala Glu Lys Phe Arg Gln Lys Ala Ser Ile His Glu Ala Trp Thr Asp
420 425 430

Gly Lys Glu Ala Met Leu Lys His Arg Asp Tyr Glu Thr Ala Thr Leu
435 440 445

Ser Asp Ile Lys Ala Leu Ile Arg Lys His Glu Ala Phe Glu Ser Asp
450 455 460

Leu Ala Ala His Gln Asp Arg Val Glu Gln Ile Ala Ala Ser Ala Gln
465 470 475 480

Glu Leu Asn Glu Leu Asp Tyr Tyr Asp Ser His Asn Val Asn Thr Arg
485 490 495

Cys Gln Lys Ile Cys Asp Gln Trp Asp Ala Leu Gly Ser Leu Thr His
500 505 510

Ser Arg Arg Glu Ala Leu Glu Lys Thr Glu Lys Gln Leu Glu Ala Ile
515 520 525

Ile Asp Gln Leu His Leu Glu Tyr Ala Lys Pro Ala Ala Pro Phe Asn
530 535 540

Asn Trp Met Glu Ser Ala Met Glu Asp Leu Gln Asp Met Phe Ile Val
545 550 555 560

His Thr Ile Glu Glu Ile Glu Gly Leu Ile Ser Ala His Asp Gln Phe
565 570 575

Lys Ser Thr Leu Pro Asp Ala Asp Arg Glu Arg Glu Ala Ile Leu His
580 585 590

Pro Gln Gly Gly Gln Arg Ile Ala Glu Ser Asn His Ile Lys Leu Ser
595 600 605

Gly Ser Asn Pro Tyr Thr Thr Val Thr Pro Gln Ile Ile Asn Ser Lys
610 615 620

Trp Glu Lys Val Gln Gln Leu Val Pro Lys Arg Asp His Ala Leu Leu
625 630 635 640

Glu Glu Gln Ser Lys Gln Gln Gln Ser Asn Glu His Leu Arg Arg Gln
645 650 655

Phe Ala Ser Gln Ala Asn Val Val Gly Pro Trp Ile Gln Thr Lys Met
660 665 670

Glu Glu Ile Ala Ile Ser Ile Glu Met Asn Gly Thr Leu Glu Asp Gln
675 680 685

Leu Ser His Leu Lys Gln Tyr Glu Arg Ser Ile Val Asp Tyr Lys Pro
690 695 700

Asn Leu Asp Leu Leu Glu Gln Gln His Gln Leu Ile Gln Glu Ala Leu
705 710 715 720

Ile Phe Asp Asn Lys His Thr Asn Tyr Thr Met Glu His Ile Arg Val
725 730 735

Gly Trp Glu Gln Leu Leu Thr Thr Ile Ala Arg Thr Ile Asn Glu Val
740 745 750

Glu Asn Gln Ile Leu Thr Arg Asp Ala Lys Gly Ile Ser Gln Glu Gln
755 760 765

Met Gln Glu Phe Arg Ala Ser Phe Asn His Phe Asp Lys Asp His Gly
770 775 780

Gly Ala Leu Gly Arg Gly Val Gln Gly Leu Pro His Gln Pro Gly Leu
785 790 795 800

Arg Arg Gly Glu Arg Pro Ala Gly Glu Ala Glu Phe Asn Arg Ile Met
805 810 815

Ser Leu Val Asp Pro Asn His Ser Gly Leu Val Thr Phe Gln Ala Phe
820 825 830

Ile Asp Phe Met Ser Arg Glu Thr Thr Asp Thr Asp Thr Ala Asp Gln
835 840 845

Val Ile Thr Ser Phe Lys Val Leu Ala Gly Asp Lys Asn Phe Ile Thr
 850 855 860

Ala Glu Glu Leu Arg Arg Glu Leu Pro Pro Asp Gln Ala Glu Tyr Cys
 865 870 875 880

Ile Ala Arg Met Ala Pro Tyr Gln Gly Pro Asp Gly Val Arg Gly Ala
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Leu Asp Tyr Lys Ser Phe Ser Thr Ala Leu Tyr Gly Glu Ser Asp Leu
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<211> 2874

<212> DNA

<213> Human

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 cgaccctgtc accaacctga acaatgcctt cgaagtggct gagaaatacc tcgacatccc 720
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 gacctatgtg tccagcttct accatgcctt ttcaggagcg cagaaggctg aaactgccgc 840
 caaccggatc tgtaagggtc tggctgtcaa ccaagagaac gagcacctga tggaggacta 900

B!
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BI
Cont

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<211> 883

<212> PRT

<213> Human

<400> 10

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Cys Asn Ser His Leu Arg Lys Ala Gly Thr Gln Ile Glu Asn Ile Asp
 35 40 45

Glu Asp Phe Arg Asp Gly Leu Lys Leu Met Leu Leu Glu Val Ile
 50 55 60

Ser Gly Glu Arg Leu Pro Lys Pro Glu Arg Gly Lys Met Arg Val His
 65 70 75 80

Lys Ile Asn Asn Val Asn Lys Ala Leu Asp Phe Ile Ala Ser Lys Gly
 85 90 95

Val Lys Leu Val Ser Ile Gly Ala Glu Glu Ile Val Asp Gly Asn Ala
 100 105 110

Lys Met Thr Leu Gly Met Ile Trp Thr Ile Ile Leu Arg Phe Ala Ile
 115 120 125

Gln Asp Ile Ser Val Glu Glu Thr Ser Ala Lys Glu Gly Leu Leu Leu
 130 135 140

B1
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Trp Cys Gln Arg Lys Thr Ala Pro Tyr Lys Asn Val Asn Val Gln Asn
145 150 155 160

Phe His Ile Ser Trp Lys Asp Gly Leu Ala Phe Asn Ala Leu Ile His
165 170 175

Arg His Arg Pro Glu Leu Ile Glu Tyr Asp Lys Leu Arg Lys Asp Asp
180 185 190

Pro Val Thr Asn Leu Asn Asn Ala Phe Glu Val Ala Glu Lys Tyr Leu
195 200 205

Asp Ile Pro Lys Met Leu Asp Ala Glu Asp Ile Val Asn Thr Ala Arg
210 215 220

Pro Asp Glu Lys Ala Ile Met Thr Tyr Val Ser Ser Phe Tyr His Ala
225 230 235 240

Phe Ser Gly Ala Gln Lys Ala Glu Thr Ala Ala Asn Arg Ile Cys Lys
245 250 255

Val Leu Ala Val Asn Gln Glu Asn Glu His Leu Met Glu Asp Tyr Glu
260 265 270

Lys Leu Ala Ser Asp Leu Leu Glu Trp Ile Arg Arg Thr Ile Pro Trp
275 280 285

Leu Glu Asp Arg Val Pro Gln Lys Thr Ile Gln Glu Met Gln Gln Lys
290 295 300

Leu Glu Asp Phe Arg Asp Tyr Arg Arg Val His Lys Pro Pro Lys Val
305 310 315 320

Gln Glu Lys Cys Gln Leu Glu Ile Asn Phe Asn Thr Leu Gln Thr Lys
325 330 335

Leu Arg Leu Ser Asn Arg Pro Ala Phe Met Pro Ser Glu Asp Lys Met
340 345 350

Val Ser Asp Ile Asn Asn Gly Trp Gln His Leu Glu Gln Ala Glu Lys
355 360 365

31
Cont.

Gly Tyr Glu Glu Trp Leu Leu Asn Glu Ile Arg Arg Leu Glu Arg Leu
370 375 380

Asp His Leu Ala Glu Lys Phe Arg Gln Lys Ala Ser Ile His Glu Trp
385 390 395 400

Thr Asp Gly Lys Glu Ala Met Leu Lys His Arg Asp Tyr Glu Thr Ala
405 410 415

Thr Leu Ser Asp Ile Lys Ala Leu Ile Arg Lys His Glu Ala Phe Glu
420 425 430

Ser Asp Leu Ala Ala His Gln Asp Arg Val Glu Gln Ile Ala Ala Ile
435 440 445

Ala Gln Glu Leu Asn Glu Leu Asp Tyr Tyr Asp Ser His Asn Val Asn
450 455 460

Thr Arg Cys Gln Lys Ile Cys Asp Gln Trp Asp Ala Leu Gly Ser Leu
465 470 475 480

Thr His Ser Arg Arg Glu Ala Leu Glu Lys Thr Glu Lys Gln Leu Glu
485 490 495

Ala Ile Asp Gln Leu His Leu Glu Tyr Ala Lys Arg Ala Ala Pro Phe
500 505 510

Asn Asn Trp Met Glu Ser Ala Met Glu Asp Leu Gln Asp Met Phe Ile
515 520 525

Val His Thr Ile Glu Glu Ile Glu Gly Leu Ile Ser Ala His Asp Gln
530 535 540

Phe Lys Ser Thr Leu Pro Asp Ala Asp Arg Glu Arg Glu Ala Ile Leu
545 550 555 560

Ala Ile His Lys Glu Ala Gln Arg Ile Ala Glu Ser Asn His Ile Lys
565 570 575

Leu Ser Gly Ser Asn Pro Tyr Thr Thr Val Thr Pro Gln Ile Ile Asn
580 585 590

B!
Cont

Ser Lys Trp Glu Lys Val Gln Gln Leu Val Pro Lys Arg Asp His Ala
595 600 605

Leu Leu Glu Glu Gln Ser Lys Gln Gln Ser Asn Glu His Leu Arg Arg
610 615 620

Gln Phe Ala Ser Gln Ala Asn Val Val Gly Pro Trp Ile Gln Thr Lys
625 630 635 640

Met Glu Glu Ile Gly Arg Ile Ser Ile Glu Met Asn Gly Thr Leu Glu
645 650 655

Asp Gln Leu Ser His Leu Lys Gln Tyr Glu Arg Ser Ile Val Asp Tyr
660 665 670

Lys Pro Asn Leu Asp Leu Leu Glu Gln Gln His Gln Leu Ile Gln Glu
675 680 685

Ala Leu Ile Phe Asp Asn Lys His Thr Asn Tyr Thr Met Glu His Ile
690 695 700

Arg Val Gly Trp Glu Gln Leu Leu Thr Thr Ile Ala Arg Thr Ile Asn
705 710 715 720

Glu Val Glu Asn Gln Ile Leu Thr Arg Asp Ala Lys Gly Ile Ser Gln
725 730 735

Glu Gln Met Gln Glu Phe Arg Ala Ser Phe Asn His Phe Asp Lys Asp
740 745 750

His Gly Gly Ala Leu Gly Pro Glu Glu Phe Lys Ala Cys Leu Ile Ser
755 760 765

Leu Gly Tyr Asp Val Glu Asn Asp Arg Gln Gly Glu Ala Glu Phe Asn
770 775 780

Arg Ile Met Ser Leu Val Asp Pro Asn His Ser Gly Leu Val Thr Phe
785 790 795 800

Gln Ala Phe Ile Asp Phe Met Ser Arg Glu Thr Thr Asp Thr Asp Thr
805 810 815

Ala Asp Gln Val Ile Ala Ser Phe Lys Val Leu Ala Gly Asp Lys Asn
 820 825 830

Phe Ile Thr Ala Glu Glu Leu Arg Arg Glu Leu Pro Pro Asp Gln Ala
 835 840 845

Glu Tyr Cys Ile Ala Arg Met Ala Pro Tyr Gln Gly Pro Asp Ala Val
 850 855 860

Pro Gly Ala Leu Asp Tyr Lys Ser Phe Ser Thr Ala Leu Tyr Gly Glu
 865 870 875 880

Ser Asp Leu

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<211> 1828

<212> DNA

<213> Human

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B1
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<211> 435

<212> PRT

<213> Human

<400> 12

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Cont.

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Asn Ile Ala Arg Thr Ser Phe Phe His Val Lys Arg Ser Asn Ile Trp
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Leu Ala Ala Val Thr Lys Gln Asn Val Asn Ala Ala Met Val Phe Glu
 65 70 75 80

Phe Leu Tyr Lys Met Cys Asp Val Met Ala Ala Tyr Phe Gly Lys Ile
 85 90 95

Ser Glu Glu Asn Ile Lys Asn Asn Phe Leu Leu Ile Tyr Glu Leu Leu
 100 105 110

Asp Glu Ile Leu Asp Phe Gly Tyr Pro Gln Asn Ser Glu Thr Gly Ala
 115 120 125

Leu Lys Thr Phe Ile Thr Gln Gln Gly Ile Lys Ser Gln His Gln Thr
 130 135 140

Lys Glu Glu Gln Ser Gln Ile Thr Ser Gln Val Thr Gly Gln Ile Gly
 145 150 155 160

Trp Arg Arg Glu Gly Ile Lys Tyr Arg Arg Asn Glu Leu Phe Leu Asp
 165 170 175

Val Leu Glu Ser Val Asn Leu Leu Met Ser Pro Gln Gly Gln Val Leu
 180 185 190

Ser Ala His Val Ser Gly Arg Val Val Met Lys Ser Tyr Leu Ser Gly
 195 200 205

Met Pro Glu Cys Lys Phe Gly Met Asn Asp Lys Ile Val Ile Glu Lys
 210 215 220

Gln Gly Lys Gly Thr Ala Asp Glu Thr Ser Lys Ser Gly Lys Gln Ser
 225 230 235 240

Ile Ala Ile Asp Asp Cys Thr Phe His Gln Cys Val Arg Leu Ser Lys
 245 250 255

Phe Asp Ser Glu Arg Ser Ile Ser Phe Ile Pro Pro Asp Gly Glu Phe
 260 265 270

Glu Leu Met Arg Tyr Arg Thr Thr Lys Asp Ile Ile Leu Pro Phe Arg
 275 280 285

Val Ile Pro Leu Val Arg Glu Val Gly Arg Thr Lys Leu Glu Val Lys
 290 295 300

Val Val Ile Lys Ser Asn Phe Lys Pro Ser Leu Leu Ala Gln Lys Ile
 305 310 315 320

Glu Val Arg Ile Pro Thr Pro Leu Asn Thr Ser Gly Val Gln Val Ile
 325 330 335

Cys Met Lys Gly Lys Ala Lys Tyr Lys Ala Ser Glu Asn Ala Ile Val
 340 345 350

Trp Lys Ile Lys Arg Met Ala Gly Met Lys Glu Ser Gln Ile Ser Ala
 355 360 365

Glu Ile Glu Leu Leu Pro Thr Asn Asp Lys Lys Lys Trp Ala Arg Pro
 370 375 380

Pro Ile Ser Met Asn Phe Glu Val Pro Phe Ala Pro Ser Gly Leu Lys
 385 390 395 400

Val Arg Tyr Leu Lys Val Phe Glu Pro Lys Leu Asn Tyr Ser Asp His
 405 410 415

Asp Val Ile Lys Trp Val Arg Tyr Ile Gly Arg Ser Gly Ile Tyr Glu
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Thr Arg Cys
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<211> 1764

<212> DNA

<213> Human

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B1
Cont.

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<210> 14

<211> 333

<212> PRT

<213> Human

<400> 14

Met Pro Leu Gly Leu Gly Arg Arg Lys Lys Ala Pro Pro Leu Val Glu
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Asn Glu Glu Ala Glu Pro Gly Arg Gly Gly Leu Gly Val Gly Glu Pro
 20 25 30

Gly Pro Leu Gly Gly Gly Gly Ser Gly Gly Pro Gln Met Gly Leu Pro
 35 40 45

Pro Pro Pro Pro Ala Leu Arg Pro Arg Leu Val Phe His Thr Gln Leu
 50 55 60

Ala His Gly Ser Pro Thr Gly Arg Ile Glu Gly Phe Thr Asn Val Lys
 65 70 75 80

Glu Leu Tyr Gly Lys Ile Ala Glu Ala Phe Arg Leu Pro Thr Ala Glu
 85 90 95

Val Met Phe Cys Thr Leu Asn Thr His Lys Val Asp Met Asp Lys Leu
 100 105 110

Leu Gly Gly Gln Ile Gly Leu Glu Asp Phe Ile Phe Ala His Val Lys
 115 120 125

Gly Gln Arg Lys Glu Val Glu Val Phe Lys Ser Glu Asp Ala Leu Gly
 130 135 140

Leu Thr Ile Thr Asp Asn Gly Ala Gly Tyr Ala Phe Ile Lys Arg Ile
 145 150 155 160

B1
 Cont.

Lys Glu Gly Ser Val Ile Asp His Ile His Leu Ile Ser Val Gly Asp
165 170 175

Met Ile Glu Ala Ile Asn Gly Gln Ser Leu Leu Gly Cys Arg His Tyr
180 185 190

Glu Val Ala Arg Leu Leu Lys Glu Leu Pro Arg Gly Arg Thr Phe Thr
195 200 205

Leu Lys Leu Thr Glu Pro Arg Lys Ala Phe Asp Met Ile Ser Gln Arg
210 215 220

Ser Ala Gly Gly Arg Pro Gly Ser Gly Pro Gln Leu Gly Thr Gly Arg
225 230 235 240

Gly Thr Leu Arg Leu Arg Ser Arg Gly Pro Ala Thr Val Glu Asp Leu
245 250 255

Pro Ser Ala Phe Glu Glu Lys Ala Ile Glu Lys Val Asp Asp Leu Leu
260 265 270

Glu Ser Tyr Met Gly Ile Arg Asp Thr Glu Leu Ala Ala Thr Met Val
275 280 285

Glu Leu Gly Lys Asp Lys Arg Asn Pro Asp Glu Leu Ala Glu Ala Leu
290 295 300

Asp Glu Arg Leu Gly Asp Phe Ala Phe Pro Asp Glu Phe Val Phe Asp
305 310 315 320

Val Trp Gly Ala Ile Gly Asp Ala Lys Val Gly Arg Tyr
325 330

<210> 15

<211> 1318

<212> DNA

<213> Human

<220>

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<221> misc_feature

<222> (23)..(23)

<223> Where n = unknown

<220>

<221> misc_feature

<222> (42)..(42)

<223> Where n = unknown

<220>

<221> misc_feature

<222> (48)..(48)

<223> Where n = unknown

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<221> misc_feature

<222> (1105)..(1105)

<223> Where n = unknown

<400> 15

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<210> 16

<211> 196

<212> PRT

<213> Human

<400> 16

Met Phe Pro Gln Ser Arg His Ser Gly Ser Ser His Leu Pro Gln Gln
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Leu Lys Phe Thr Thr Ser Asp Ser Cys Asp Arg Ile Lys Asp Glu Phe
 20 25 30

Gln Leu Leu Gln Ala Gln Tyr His Ser Leu Lys Leu Glu Cys Asp Lys
 35 40 45

Leu Ala Ser Glu Lys Ser Glu Met Gln Arg His Tyr Val Met Tyr Tyr
 50 55 60

Glu Met Ser Tyr Gly Leu Asn Ile Glu Met His Lys Gln Ala Glu Ile
 65 70 75 80

Val Lys Arg Leu Asn Gly Ile Cys Ala Gln Val Leu Pro Tyr Leu Ser
85 90 95

Gln Glu His Gln Gln Gln Val Leu Gly Ala Ile Glu Arg Ala Lys Gln
100 105 110

Val Thr Ala Pro Glu Leu Asn Ser Ile Ile Arg Gln Gln Leu Gln Ala
115 120 125

His Gln Leu Ser Gln Leu Gln Ala Leu Ala Leu Pro Leu Thr Pro Leu
130 135 140

Pro Val Gly Leu Gln Pro Pro Ser Leu Pro Ala Val Ser Ala Gly Thr
145 150 155 160

Gly Leu Leu Ser Leu Ser Ala Leu Gly Ser Gln Ala His Leu Ser Lys
165 170 175

Glu Asp Lys Asn Gly His Asp Gly Asp Thr His Gln Glu Asp Asp Gly
180 185 190

Glu Lys Ser Asp
195

<210> 17

<211> 1264

<212> DNA

<213> Human

<220>

<221> misc_feature

<222> (23)..(23)

<223> Where n = unknown

<220>

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<222> (42) .. (42)

<223> Where n = unknown

<400> 17

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actgcaagct cagtaccaca gcctcaagct cgaatgtgac aagttggcca gtgagaagtc 240
agagatgcag cgtcactatg tgatgtacta cgagatgtcc tacggcttga acatcgagat 300
gcacaaacag gctgagatcg tcaaaaggct gaacgggatt tgtgcccagg tctgcacct 360
cctctcccaa gagcaccagc agcaggctctt gggagccatt gagagggcca agcaggctac 420
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gcaggccctg gccctgcctt tgacccact acccgtgggg ctgcagccgc cttcgtgcc 540
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gtcggattag cagggggccg ggacaggag gttgggagg gggacagagg ggagacagag 720
gcacggagag aaaggaatgt ttagcacaag acacagcgga gtcgggatt ggctaactc 780
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tact 1264

<210> 18

<211> 197

<212> PRT

<213> Human

<400> 18

Met Met Phe Pro Gln Ser Arg His Ser Gly Ser Ser His Leu Pro Gln
1 5 10 15

Gln Leu Lys Phe Thr Thr Ser Asp Ser Cys Asp Arg Ile Lys Asp Glu
20 25 30

Phe Gln Leu Leu Gln Ala Gln Tyr His Ser Leu Lys Leu Glu Cys Asp
35 40 45

Lys Leu Ala Ser Glu Lys Ser Glu Met Gln Arg His Tyr Val Met Tyr
50 55 60

Tyr Glu Met Ser Tyr Gly Leu Asn Ile Glu Met His Lys Gln Ala Glu
65 70 75 80

Ile Val Lys Arg Leu Asn Gly Ile Cys Ala Gln Val Leu Pro Tyr Leu
85 90 95

Ser Gln Glu His Gln Gln Gln Val Leu Gly Ala Ile Glu Arg Ala Lys
100 105 110

Gln Val Thr Ala Pro Glu Leu Asn Ser Ile Ile Arg Gln Gln Leu Gln
115 120 125

Ala His Gln Leu Ser Gln Leu Gln Ala Leu Ala Leu Pro Leu Thr Pro
130 135 140

Leu Pro Val Gly Leu Gln Pro Pro Ser Leu Pro Ala Val Ser Ala Gly
145 150 155 160

Thr Gly Leu Leu Ser Leu Ser Ala Leu Gly Ser Gln Ala His Leu Ser
165 170 175

Lys Glu Asp Lys Asn Gly His Asp Gly Asp Thr His Gln Glu Asp Asp
180 185 190

Gly Glu Lys Ser Asp
195

<210> 19

<211> 1809

<212> DNA

<213> Human

<400> 19

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aacgagggcg tgtataatgg aagctgggga ggccggggag aggttattac gacctattgc 180
cccgctaaca acgagccaat agcaagagtc cgacaggcca gtgtggcaga ctatgaagaa 240
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atcacggcat tcaatttccc tgtggcagtg tatggttga acaacgcat cgccatgatc 600
tgtggaaatg tctgcctctg gaaaggagct ccaaccactt ccctcattag tgtggctgtc 660
acaaagataa tagccaaggt tctggaggac aacaagctgc ctggtgcaat ttgttccttg 720
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gtaaaacagg gactttcaag tagcatcttt accaaagatc tgggcagaat ctttcgctgg 1380

B1
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 cctctggccc aaggaatcaa gtttcagtaa aggtgtttta gatgaacatc ccttaatttg 1620
 aggtgttcca gcagctgttt ttggagaaga caaagaagat taaagttttc cctgaataaa 1680
 tgcattatta tgactgtgac agtgactaat cccctatga ccccaaagcc ctgattaaat 1740
 caagagattc cttttttaa aatcaaaaata aaattgttac aacatagcca tagttactaa 1800
 aaaaaaaaaa 1809

<210> 20

<211> 511

<212> PRT

<213> Human

<400> 20

Met Ser Thr Leu Leu Ile Asn Gln Pro Gln Tyr Ala Trp Leu Lys Glu
1 5 10 15

Leu Gly Leu Arg Glu Glu Asn Glu Gly Val Tyr Asn Gly Ser Trp Gly
20 25 30

Gly Arg Gly Glu Val Ile Thr Thr Tyr Cys Pro Ala Asn Asn Glu Pro
35 40 45

Ile Ala Arg Val Arg Gln Ala Ser Val Ala Asp Tyr Glu Glu Thr Val
50 55 60

Lys Lys Ala Arg Glu Ala Trp Lys Ile Trp Ala Asp Ile Pro Ala Pro
65 70 75 80

Lys Arg Gly Glu Ile Val Arg Gln Ile Gly Asp Ala Leu Arg Glu Lys
85 90 95

Ile Gln Val Leu Gly Ser Leu Val Ser Leu Glu Met Gly Lys Ile Leu
100 105 110

Val Glu Gly Val Gly Glu Val Gln Glu Tyr Val Asp Ile Cys Asp Tyr
115 120 125

Ala Val Gly Leu Ser Arg Met Ile Gly Gly Pro Ile Leu Pro Ser Glu
130 135 140

Arg Ser Gly His Ala Leu Ile Glu Gln Trp Asn Pro Val Gly Leu Val
145 150 155 160

Gly Ile Ile Thr Ala Phe Asn Phe Pro Val Ala Val Tyr Gly Trp Asn
165 170 175

Asn Ala Ile Ala Met Ile Cys Gly Asn Val Cys Leu Trp Lys Gly Ala
180 185 190

Pro Thr Thr Ser Leu Ile Ser Val Ala Val Thr Lys Ile Ile Ala Lys
195 200 205

Val Leu Glu Asp Asn Lys Leu Pro Gly Ala Ile Cys Ser Leu Thr Cys
210 215 220

Gly Gly Ala Asp Ile Gly Thr Ala Met Ala Lys Asp Glu Arg Val Asn
225 230 235 240

Leu Leu Ser Phe Thr Gly Ser Thr Gln Val Gly Lys Gln Val Gly Leu
245 250 255

Met Val Gln Glu Arg Phe Gly Arg Ser Leu Leu Glu Leu Gly Gly Asn
260 265 270

Asn Ala Ile Ile Ala Phe Glu Asp Ala Asp Leu Ser Leu Val Val Pro
275 280 285

Ser Ala Leu Phe Ala Ala Val Gly Thr Ala Gly Gln Arg Cys Thr Thr
290 295 300

Ala Arg Arg Leu Phe Ile His Glu Ser Ile His Asp Glu Val Val Asn
305 310 315 320

Arg Leu Lys Lys Ala Tyr Ala Gln Ile Arg Val Gly Asn Pro Trp Asp
325 330 335

Pro Asn Val Leu Tyr Gly Pro Leu His Thr Lys Gln Ala Val Ser Met
340 345 350

Phe Leu Gly Ala Val Glu Glu Ala Lys Lys Glu Gly Gly Thr Val Val
 355 360 365

Tyr Gly Gly Lys Val Met Asp Arg Pro Gly Asn Tyr Val Glu Pro Thr
 370 375 380

Ile Val Thr Gly Leu Gly His Asp Ala Ser Ile Ala His Thr Glu Thr
 385 390 395 400

Phe Ala Pro Ile Leu Tyr Val Phe Lys Phe Lys Asn Glu Glu Glu Val
 405 410 415

Phe Ala Trp Asn Asn Glu Val Lys Gln Gly Leu Ser Ser Ser Ile Phe
 420 425 430

Thr Lys Asp Leu Gly Arg Ile Phe Arg Trp Leu Gly Pro Lys Gly Ser
 435 440 445

Asp Cys Gly Ile Val Asn Val Asn Ile Pro Thr Ser Gly Ala Glu Ile
 450 455 460

Gly Gly Ala Phe Gly Gly Glu Lys His Thr Gly Gly Gly Arg Glu Ser
 465 470 475 480

Gly Ser Asp Ala Trp Lys Gln Tyr Met Arg Arg Ser Thr Cys Thr Ile
 485 490 495

Asn Tyr Ser Lys Asp Leu Pro Leu Ala Gln Gly Ile Lys Phe Gln
 500 505 510

<210> 21

<211> 1428

<212> DNA

<213> Human

<400> 21

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acgcctggaa caaggaccgc acccagattg ccatctgccc caacaaccat gaggtgcata 180

B1
cont

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<210> 22

<211> 372

<212> PRT

<213> Human

<400> 22

Met	Ala	Tyr	His	Ser	Phe	Leu	Val	Glu	Pro	Ile	Ser	Cys	His	Ala	Trp
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20 25 30

His Ile Tyr Glu Lys Ser Gly Ala Lys Trp Thr Lys Val His Glu Leu
35 40 45

Lys Glu His Asn Gly Gln Val Thr Gly Ile Asp Trp Ala Pro Glu Ser
50 55 60

Asn Arg Ile Val Thr Cys Gly Thr Asp Arg Asn Ala Tyr Val Trp Thr
65 70 75 80

Leu Lys Gly Arg Thr Trp Lys Pro Thr Leu Val Ile Leu Arg Ile Asn
85 90 95

Arg Ala Ala Arg Cys Val Arg Trp Ala Pro Asn Glu Asn Lys Phe Ala
100 105 110

Val Gly Ser Gly Ser Arg Val Ile Ser Ile Cys Tyr Phe Glu Gln Glu
115 120 125

Asn Asp Trp Trp Val Cys Lys His Ile Lys Lys Pro Ile Arg Ser Thr
130 135 140

Val Leu Ser Leu Asp Trp His Pro Asn Asn Val Leu Leu Ala Ala Gly
145 150 155 160

Ser Cys Asp Phe Lys Cys Arg Ile Phe Ser Ala Tyr Ile Lys Glu Val
165 170 175

Glu Glu Arg Pro Ala Pro Thr Pro Trp Gly Ser Lys Met Pro Phe Gly
180 185 190

Glu Leu Met Phe Glu Ser Ser Ser Ser Cys Gly Trp Val His Gly Val
195 200 205

Cys Phe Ser Ala Ser Gly Ser Arg Val Ala Trp Val Ser His Asp, Ser
210 215 220

Thr Val Cys Leu Ala Asp Ala Asp Lys Lys Met Ala Val Ala Thr Leu
225 230 235 240

Ala Ser Glu Thr Leu Pro Leu Leu Ala Leu Thr Phe Ile Thr Asp Asn
245 250 255

B1
Cont.

Ser Leu Val Ala Ala Gly His Asp Cys Phe Pro Val Leu Phe Thr Tyr
 260 265 270

Asp Ala Ala Ala Gly Met Leu Ser Phe Gly Gly Arg Leu Asp Val Pro
 275 280 285

Lys Gln Ser Ser Gln Arg Gly Leu Thr Ala Arg Glu Arg Phe Gln Asn
 290 295 300

Leu Asp Lys Lys Ala Ser Ser Glu Gly Gly Thr Ala Ala Gly Ala Gly
 305 310 315 320

Leu Asp Ser Leu His Lys Asn Ser Val Ser Gln Ile Ser Val Leu Ser
 325 330 335

Gly Gly Lys Ala Lys Cys Ser Gln Phe Cys Thr Thr Gly Met Asp Gly
 340 345 350

Gly Met Ser Ile Trp Asp Val Lys Ser Leu Glu Ser Ala Leu Lys Asp
 355 360 365

Leu Lys Ile Lys
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<210> 23

<211> 1373

<212> DNA

<213> Human

<400> 23
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B1
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<210> 24

<211> 230

<212> PRT

<213> Human

<400> 24

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Tyr His Thr Thr Asp Ala Ser Leu Arg Lys Tyr Phe Glu Gly Phe Gly
 35 40 45

Asp Ile Glu Glu Ala Val Val Ile Thr Asp Arg Gln Thr Gly Lys Ser
50 55 60

Arg Gly Tyr Gly Phe Val Thr Met Ala Asp Arg Ala Ala Ala Glu Arg
65 70 75 80

Ala Cys Lys Asp Pro Asn Pro Ile Ile Asp Gly Arg Lys Ala Asn Val
85 90 95

Asn Leu Ala Tyr Leu Gly Ala Lys Pro Trp Cys Leu Gln Thr Gly Phe
100 105 110

Ala Ile Gly Val Gln Gln Leu His Pro Thr Leu Ile Gln Arg Thr Tyr
115 120 125

Gly Leu Thr Pro His Tyr Ile Tyr Pro Pro Ala Ile Val Gln Pro Ser
130 135 140

Val Val Ile Pro Ala Ala Ala Pro Val Pro Ser Leu Ser Ser Pro Tyr
145 150 155 160

Ile Glu Tyr Thr Pro Ala Ser Pro Val Tyr Ala Gln Tyr Pro Pro Ala
165 170 175

Thr Tyr Asp Gln Tyr Pro Tyr Ala Ala Ser Pro Ala Thr Ala Asp Ser
180 185 190

Phe Val Gly Tyr Ser Tyr Pro Ala Ala Val His Gln Ala Leu Ser Ala
195 200 205

Ala Ala Pro Ala Gly Thr Thr Phe Val Gln Tyr Gln Ala Pro Gln Leu
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Gln Pro Asp Arg Met Gln
225 230

<210> 25

<211> 1439

<212> DNA

<213> Human

<400> 25
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<210> 26

<211> 230

<212> PRT

<213> Human

B1
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<400> 26

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Gly Lys Lys Lys Gly Thr Thr Phe Thr Lys Ile Phe Val Gly Gly Leu
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Pro Tyr His Thr Thr Asp Ala Ser Leu Arg Lys Tyr Phe Glu Gly Phe
35 40 45

Gly Asp Ile Glu Glu Ala Val Val Ile Thr Asp Arg Gln Thr Gly Lys
50 55 60

Ser Arg Gly Tyr Gly Phe Val Thr Met Ala Asp Arg Ala Ala Ala Glu
65 70 75 80

Arg Ala Cys Lys Asp Pro Asn Pro Ile Ile Asp Gly Arg Lys Ala Asn
85 90 95

Val Asn Leu Ala Tyr Leu Gly Ala Lys Pro Trp Cys Leu Gln Thr Gly
100 105 110

Phe Ala Ile Gly Val Gln Gln Leu His Pro Thr Leu Ile Gln Arg Thr
115 120 125

Tyr Gly Leu Thr Pro His Tyr Ile Tyr Pro Pro Ala Ile Val Gln Pro
130 135 140

Ser Val Val Ile Pro Ala Ala Pro Val Pro Ser Leu Ser Ser Pro Tyr
145 150 155 160

Ile Glu Tyr Thr Pro Ala Ser Pro Val Tyr Ala Gln Tyr Pro Pro Ala
165 170 175

Thr Tyr Asp Gln Tyr Pro Tyr Ala Ala Ser Pro Ala Thr Ala Asp Ser
180 185 190

Phe Val Gly Tyr Ser Tyr Pro Ala Ala Val His Gln Ala Leu Ser Ala
195 200 205

Ala Ala Pro Ala Gly Thr Thr Phe Val Gln Tyr Gln Ala Pro Gln Leu
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Gln Pro Asp Arg Met Gln
 225 230

<210> 27

<211> 2029

<212> DNA

<213> Human

<400> 27

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B1
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<210> 28

<211> 572

<212> PRT

<213> Human

<400> 28

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Ser Ser Thr Pro Leu Ser Pro Thr Arg Ile Thr Arg Leu Gln Glu Lys
20 25 30

Glu Asp Leu Gln Glu Leu Asn Asp Arg Leu Ala Val Tyr Ile Asp Arg
35 40 45

Val Arg Ser Leu Glu Thr Glu Asn Ala Gly Leu Arg Leu Arg Ile Thr
50 55 60

Glu Ser Glu Glu Val Val Ser Arg Glu Val Ser Gly Ile Lys Ala Ala
65 70 75 80

Tyr Glu Ala Glu Leu Gly Asp Ala Arg Lys Thr Leu Asp Ser Val Ala
85 90 95

Lys Glu Arg Ala Arg Leu Gln Leu Glu Leu Ser Lys Val Arg Glu Glu
100 105 110

Phe Lys Glu Leu Lys Ala Arg Asn Thr Lys Lys Glu Gly Asp Leu Ile
115 120 125

Ala Ala Gln Ala Arg Leu Lys Asp Leu Glu Ala Leu Leu Asn Ser Lys
130 135 140

Glu Ala Ala Leu Ser Thr Ala Leu Ser Glu Lys Arg Thr Leu Glu Gly
145 150 155 160

Glu Leu His Asp Leu Arg Gly Gln Val Ala Lys Leu Glu Ala Ala Leu
165 170 175

Gly Glu Ala Lys Lys Gln Leu Gln Asp Glu Met Leu Arg Arg Val Asp
180 185 190

Ala Glu Asn Arg Leu Gln Thr Met Lys Glu Glu Leu Asp Phe Gln Lys
195 200 205

Asn Ile Tyr Ser Glu Glu Leu Arg Glu Thr Lys Arg Arg His Glu Thr
210 215 220

Arg Leu Val Glu Ile Asp Asn Gly Lys Gln Arg Glu Phe Glu Ser Arg
225 230 235 240

Leu Ala Asp Ala Leu Gln Glu Leu Arg Ala Gln His Glu Asp Gln Val
245 250 255

Glu Gln Tyr Lys Lys Glu Leu Glu Lys Thr Tyr Ser Ala Lys Leu Asp
260 265 270

Asn Ala Arg Gln Ser Ala Glu Arg Asn Ser Asn Leu Val Gly Ala Ala
275 280 285

His Glu Glu Leu Gln Gln Ser Arg Ile Arg Ile Asp Ser Leu Ser Ala
290 295 300

Gln Leu Ser Gln Leu Gln Lys Gln Leu Ala Ala Lys Glu Ala Lys Leu
305 310 315 320

Arg Asp Leu Glu Asp Ser Leu Ala Arg Glu Arg Asp Thr Ser Arg Arg
325 330 335

Leu Leu Ala Glu Lys Glu Arg Glu Met Ala Glu Met Arg Ala Arg Met
340 345 350

Gln Gln Gln Leu Asp Glu Tyr Gln Glu Leu Leu Asp Ile Lys Leu Ala
355 360 365

Leu Asp Met Glu Ile His Ala Tyr Arg Lys Leu Leu Glu Gly Glu Glu
370 375 380

Glu Arg Leu Arg Leu Ser Pro Ser Pro Thr Ser Gln Arg Ser Arg Gly
385 390 395 400

Arg Ala Ser Ser His Ser Ser Gln Thr Gln Gly Gly Gly Ser Val Thr
405 410 415

Lys Lys Arg Lys Leu Glu Ser Thr Glu Ser Arg Ser Ser Phe Ser Gln
420 425 430

His Ala Arg Thr Ser Gly Arg Val Ala Val Glu Glu Val Asp Glu Glu
435 440 445

Gly Lys Phe Val Arg Leu Arg Asn Lys Ser Asn Glu Asp Gln Ser Met
450 455 460

Gly Asn Trp Gln Ile Lys Arg Gln Asn Gly Asp Asp Pro Leu Leu Thr
465 470 475 480

Tyr Arg Phe Pro Pro Lys Phe Thr Leu Lys Ala Gly Gln Val Val Thr
485 490 495

Ile Trp Ala Ala Gly Ala Gly Ala Thr His Ser Pro Pro Thr Asp Leu
500 505 510

Val Trp Lys Ala Gln Asn Thr Trp Gly Cys Gly Asn Ser Leu Arg Thr
515 520 525

Ala Leu Ile Asn Ser Thr Gly Glu Glu Val Ala Met Arg Lys Leu Val
530 535 540

Arg Ser Val Thr Val Val Glu Asp Asp Glu Asp Glu Asp Gly Asp Asp
545 550 555 560

Leu Leu His His His His Val Ser Gly Ser Arg Arg
565 570

B1
Cont